



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> PARANHOS-BACCALA, Glaucia

KOMURIAN-PRADEL, Florence

BEDIN, Frederic

SODOYER, Mireille

OTT, Catherine

MALLET, Francois

PERRON, Herve

MANDRAND, Bernard

<120> RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES

<130> 103514

<140> US/09/319,156

<141> 1999-11-02

<150> PCT/FR98/01460

<151> 1998-07-07

<150> FR/97/08816

<151> 1997-07-07

<160> 45

<170> PatentIn version 3.1

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120

agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac

180

ccttcaccaa accttccact taggcattga tagcacccat cagatggcca aattattatt 240
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<223> Xaa = any amino acid

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Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
 35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
 50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
 65 70 75 80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys
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Glu Val Cys Gln Arg Asn Asn
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 Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
 35 40 45

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
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Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser
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 ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg ggggtggaatt 360
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 ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt 720
 agcaatacta tagacacaac cagctcccaa tgcatacagg gggtaacacc tcccacacga 780

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<223> Xaa = any amino acid

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Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser
          20           25           30

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Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
          35           40           45

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Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
100 105 110

Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
115 120 125

Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
130 135 140

Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu
180 185 190

His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile
305 310 315 320

Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly
325 330 335

Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
340 345 350

Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu
355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
370 375 380

Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
385 390 395 400

Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
420 425 430

Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val
435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Phe
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Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile
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Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro
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<223> n = a, g, c or t/u

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120

aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct

180

cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt	240
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<222> (46)..(46)

<223> Xaa = any amino acid

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Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg
35 40 45

Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp
50 55 60

Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe
65 70 75 80

Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val
85 90 95

Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu
100 105 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg
115 120 125

Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro
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Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly
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Ser Ser

<210> 14

<211> 21

<212> DNA

<213> MSRV

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<210> 16

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<212> DNA

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<400> 20
tggctctcaa tgggtcaaaca tacccg 26

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<211> 352

<212> PRT

<213> MSRV

<400> 22

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 20 25 30

Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr
 35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp
 50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser
 65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser
 85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn
 100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly
 115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu
 130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro
 145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe
 165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln
 180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr
 195 200 205

Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe
 210 215 220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu
 225 230 235 240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro
 245 250 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu
 260 265 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met
 275 280 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu
 290 295 300

Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser
 305 310 315 320

Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe
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Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro
 340 345 350

<210> 23

<211> 30

<212> DNA

<213> MSRV

<400> 23

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<210> 25

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<212> PRT

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 20 25 30

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 35 40 45

Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln
 50 55 60

Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn
 65 70 75 80

Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys
 85 90 95

Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn
 100 105 110

Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln
 115 120 125

Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr
 130 135 140

Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys
 145 150 155 160

Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro
 165 170 175

Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val
 180 185 190

Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys
 195 200 205

Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly
 210 215 220

Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln
 225 230 235 240

Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu
 245 250 255

Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr
 260 265 270

Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp
275 280 285

Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His
290 295 300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro
305 310 315 320

Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn
325 330 335

Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr
340 345 350

Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys
355 360 365

Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu
370 375 380

Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His
385 390 395

<210> 26

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35 40 45

Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile
50 55 60

Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val
 65 70 75 80

Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys
 85 90 95

Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro
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Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro
 115 120 125

Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn
 130 135 140

Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val
 145 150 155 160

Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu
 165 170 175

Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn
 180 185 190

Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp
 195 200 205

Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro
 210 215 220

Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu
 225 230 235 240

Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr
 245 250 255

Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp
 260 265 270

Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys
 275 280 285

Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser
 290 295 300

Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe
 305 310 315 320

Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro
 325 330 335

Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln
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Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala
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25

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<210> 29

<211> 25

<212> DNA

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<400> 29

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<211> 764

<212> DNA

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<400> 30

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tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca	180
ctgcatggtc caagattcca ttccttgga tccgtgagac caagaacccc aggtcagaga	240
acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaagc agcccgccac	300
tatcttggga gctctgggag caaggacccc aggtaacaat ttggtgacca cgaagggacc	360
tgaatccgca accatgaagg gatctccaaa gcaattggaa atgttcctcc caaggcaaaa	420
atgcccctaa gatgtattct ggagaattgg gaccaatttg accctcagac agtaagaaaa	480
aaatgactta tattcttctg cagtaccgcc ctggccacga ttcctcttc aagggggaga	540
aacctggcct cctgagggaa gtataaatta taacaccatc ttacagctag acctgttttg	600
tagaaaagga ggcaaagga gtgaagtgcc atatttacia actttctttt cattaaaaga	660
caactcgcaa ttatgttaac agtgtgattt gtgttcctac acggaagccc tcagattcta	720
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<210> 31

<211> 800

<212> DNA

<213> MSRV

<400> 31

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<211> 65

<212> PRT

<213> MSRV

<400> 32

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 20 25 30

Arg Leu Ala Thr Met Leu Glu Ala Ala His His His Phe Gly Ser Ser
 35 40 45

Pro Pro Leu Ser Trp Glu Leu Trp Glu Gln Gly Pro Gln Val Thr Ile
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Trp
 65

<210> 33

<211> 26

<212> DNA

<213> MSRV

<400> 33

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26

<210> 34

<211> 28

<212> DNA

<213> MSRV

<400> 34

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28

<210> 35

<211> 28

<212> DNA

<213> MSRV

<400> 35

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28

<210> 36

<211> 31

<212> DNA

<213> MSRV

<400> 36

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31

<210> 37
<211> 25
<212> DNA
<213> MSRV

<400> 37
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25

<210> 38
<211> 33
<212> DNA
<213> MSRV

<400> 38
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33

<210> 39
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<213> MSRV

<400> 39
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28

<210> 40
<211> 1247
<212> DNA
<213> MSRV

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<222> (1240)..(1240)

<223> n = a, g, c or t/u

<220>

<221> misc_feature

<222> (1246)..(1246)

<223> n = a, g, c or t/u

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gcctggccac aatatcctct tcaagggaga gaaacctggc ttcttgaggg aagtataaat	240
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ccttcctcaa ctaataagga ccccccttta acccaaacgg tccaaaagga gatagacaaa	480
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 <211> 1186
 <212> DNA
 <213> MSRV

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 <211> 2030
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<213> MSRV

<400> 42

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acgcggcttc	ctggaaatat	tgatgcccc	tcatatagga	gtttatctaa	gggaaactcc	180
accttcactg	cccacaccca	tatgccccgc	aactgctata	actctgccac	tctttgcatg	240
catgcaaata	ctcattattg	gacagggaaa	atgattaatc	ctagttgtcc	tggaggactt	300
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<211> 2055

<212> DNA

<213> MSRV

<400> 43

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<211> 1197

<212> DNA

<213> MSRV

<400> 44

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<210> 45

<211> 1718

<212> DNA

<213> MSRV

<400> 45

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